



warf Sequence.ST25.txt
SEQUENCE LISTING

<110> Harms, Jerome S
Splitter, Gary A
Eakle, Kurt A
Bremel, Robert D

<120> Inducible Protein Expression System

<130> 2240/3

<140> US 10/763,976

<141> 2004-01-23

<160> 65

<170> PatentIn version 3.3

<210> 1

<211> 576

<212> DNA

<213> Artificial

<220>

<223> Engineered Sequence from virus and plasmid

<220>

<221> Promoter

<222> (87)..(432)

<223> BLV Promoter

<400> 1
aggaaaccag cagcggctat ccgcgcattcc atgccccga actgcaggag tggggaggca 60
cgatggccgc tttggtcgag gcggatccta gcagaaaaat aagacttgat tcccccttaa 120
aattacaact gctagaaaat gaatggctct cccgcctttt ttgaggggaa atcatttgta 180
tgaaagatca tgccgaccta ggcggccca ccggcccgta aaccagacag agacgtcagc 240
tgccagaaaa gctggtgacg gcagctggtg gctagaatcc ccgtacctcc ccaacttccc 300
ctttccgaa aaatcccacac cctgagctgc tgacctcacc tgctgataaa ttaataaaat 360
gccggccctg tcgagttagc ggcaccagaa gcgttcttct cctgagaccc tcgtgctcag 420
ctctcggtcc tgcctcgaga agcttggat cacaagtttgc tacaaaaaag ctgaacgaga 480
aacgtaaaat gatataaata tcaatataatt aaatttagatt ttgcataaaa aacagactac 540
ataatactgt aaaacacaac atatccagtc actatg 576

<210> 2

<211> 930

<212> DNA

<213> Bovine leukemia virus

<220>

<221> CDS

<222> (1)..(930)

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Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
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tgc gac cgg tta cac gta tgg tcc agt cct cag gcc tta cag cgc ttc
Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

ctc cat gac cct acg cta acc tgg tca gaa ttg gtt gct agc agg aaa
Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

cta aga ctt gat tca ccc tta aaa tta caa ctg tta gaa aat gaa tgg
Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

ctc tcc cgc ctt ttt tga
Leu Ser Arg Leu Phe
305

<210> 3

<211> 309

<212> PRT

<213> Bovine leukemia virus

<400> 3

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

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Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

Leu Ser Arg Leu Phe
305

<210> 4

<211> 1062

<212> DNA

<213> Human T-cell lymphotropic virus type 1

<220>

<221> promoter

<222> (1)..(353)

<400> 4

atggcccaact tcccagggtt tggacagagt cttctttcg gatacccgat ctacgtttt 60

ggagacggcg actggtgccc ctgtgtacaa atctctgggg gactatgttc ggcccgccct 120

catcgtcacg ccctactggc cacctgtcca gagcatcaga tcacctggga ccccatcgat 180

ggacgcgtta tcggctcagc tctacagttc cttatccctc gactcccctc cttccccacc 240

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cagagaacct	ctaagacct	caaggcctt	acccgccaa	tcactcatac	aaccccaac	300
attccaccct	cttccctcca	ggccatgcgc	aaatactccc	cttccgaaa	tggatacatg	360
gaacccaccc	ttgggcagca	cctcccaacc	ctgtctttc	cagaccccg	actccggccc	420
caaaaacctgt	acaccctctg	gggaggctcc	gttgcgtca	tgtacctcta	ccagcttcc	480
ccccccatca	cctggccctt	cctggccac	gtgattttt	gccaccccg	ccagctcggg	540
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accacagggg	ccctaataat	tctacccgaa	gactgttgc	ccaccaccc	tttccagcct	660
gttagggcac	ccgtcacgct	aacagcctgg	caaaacggcc	tccttcgtt	ccactcaacc	720
ctcaccactc	caggccttat	ttggacattt	accgatggca	cgcctatgtat	ttccgggccc	780
tgccctaaag	atggccagcc	atcttagta	ctacagtcct	cctcccttat	atttcacaaa	840
tttcaaacca	aggcctacca	cccctcattt	ctactctcac	acggcctcat	acagtactct	900
tccttcata	atttacatct	cctgttgaa	gaatacacca	acatccccat	ttctctactt	960
tttaacaaaa	aagaggcaga	tgacaatgac	catgagcccc	aaatatcccc	cgggggctta	1020
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<210> 5
<211> 353
<212> DNA
<213> Human T-cell lymphotropic virus type 1

<400> 5
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ccggaggaca gctcagcacc agctcaggct aggcctgac gtgtccccct aaagacaat 180
cataagctca gacctccggg aagccaccgg gaaccaccca tttccctcccc atgtttgtca 240
agccgtcctc aggcgttgac gacaacccct cacctaaaa aactttcat ggcacgcata 300
cggctcaata aaataacagg agtctataaa agcgtgggga cagttcagga ggg 353

<210> 6
<211> 456
<212> DNA
<213> Human immunodeficiency virus type 1

<220>
<221> CDS
<222> (1)..(456)

<400> 6
ctg gaa ggg cta att tgg tcc caa aga aga caa gag atc ctt gat ctg 48
Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
1 5 10 15

warf Sequence.ST25.txt

tgg atc tac cac aca caa ggc tac ttc cct gat tgg cag aat tac aca Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr 20 25 30	96
cca ggg cca ggg atc aga tat cca ctg acc ttt gga tgg tgc ttc aag Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys 35 40 45	144
cta gta cca gtt gag cca gag aag gta gaa gag gcc aat gaa gga gag Leu Val Pro Val Glu Pro Glu Lys Val Glu Ala Asn Glu Gly Glu 50 55 60	192
aac aac agc ttg tta cac cct atg agc ctg cat ggg atg gag gac gcg Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala 65 70 75 80	240
gag aaa gaa gtg tta gtg tgg agg ttt gac agc aaa cta gca ttt cat Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His 85 90 95	288
cac atg gcc cga gag ctg cat ccg gag tac tac aaa gac tgc tga cat His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys His 100 105 110	336
cga gct ttc tac aag gga ctt tcc gct ggg gac ttt cca ggg agg cgt Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg Arg 115 120 125	384
ggc ctg ggc ggg act ggg gag tgg cgt ccc tca gat gct gca tat aag Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr Lys 130 135 140	432
cag ctg ctt ttt gcc tgt act ggg Gln Leu Leu Phe Ala Cys Thr Gly 145 150	456

<210> 7

<211> 110

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 7

Leu Glu Gly Leu Ile Trp Ser Gln Arg Arg Gln Glu Ile Leu Asp Leu
1 5 10 15

Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
20 25 30

Pro Gly Pro Gly Ile Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe Lys
35 40 45

Leu Val Pro Val Glu Pro Glu Lys Val Glu Ala Asn Glu Gly Glu
50 55 60

Asn Asn Ser Leu Leu His Pro Met Ser Leu His Gly Met Glu Asp Ala
65 70 75 80

warf Sequence.ST25.txt

Glu Lys Glu Val Leu Val Trp Arg Phe Asp Ser Lys Leu Ala Phe His
 85 90 95

His Met Ala Arg Glu Leu His Pro Glu Tyr Tyr Lys Asp Cys
 100 105 110

<210> 8
 <211> 41
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 8

His Arg Ala Phe Tyr Lys Gly Leu Ser Ala Gly Asp Phe Pro Gly Arg
 1 5 10 15

Arg Gly Leu Gly Gly Thr Gly Glu Trp Arg Pro Ser Asp Ala Ala Tyr
 20 25 30

Lys Gln Leu Leu Phe Ala Cys Thr Gly
 35 40

<210> 9
 <211> 306
 <212> DNA
 <213> Human immunodeficiency virus type 1

<220>
 <221> CDS
 <222> (1)..(303)

<400> 9
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 Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
 1 5 10 15

cag cct agg act gct tgt aac aat tgc tat tgt aaa aag tgt tgc ttt 96
 Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 20 25 30

cat tgc tac gcg tgt ttc aca aga aaa ggc tta ggc atc tcc tat ggc 144
 His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
 35 40 45

agg aag aag cgg aga cag cga cga aga gct cct cag gac agt cag act 192
 Arg Lys Lys Arg Arg Gln Arg Arg Ala Pro Gln Asp Ser Gln Thr
 50 55 60

cat caa gct tct cta tca aag caa ccc gcc tcc cag tcc cga ggg gac 240
 His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
 65 70 75 80

ccg aca ggc ccg acg gaa tcg aag aag aag gtg gag aga gag aca gag 288
 Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
 85 90 95

aca gat ccg ttc gat tag
Thr Asp Pro Phe Asp
100

<210> 10
<211> 101
<212> PRT
<213> Human immunodeficiency virus type 1
<400> 10

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

Pro Thr Gly Pro Thr Glu Ser Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

Thr Asp Pro Phe Asp
100

<210> 11
<211> 309
<212> PRT
<213> Bovine leukemia virus

<400> 11

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr His
35 40 45

Thr Cys Glu Thr His Arg Ile Thr Trp Thr Ala Asp Gly Arg Pro Phe
50 55 60

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Gly Leu Asn Gly Ala Leu Phe Pro Arg Leu His Val Ser Arg Asp Pro
65 70 75 80

Ala Pro Arg Ala Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Val Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

Pro Cys Pro Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Pro Phe Asn Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Leu Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp
290 295 300

Leu Ser Arg Leu Phe
305

warf Sequence.ST25.txt

<210> 12
<211> 353
<212> PRT
<213> Human T-cell lymphotropic virus type 1

<400> 12

Met Ala His Phe Pro Gly Phe Gly Gln Ser Leu Leu Phe Gly Tyr Pro
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Val Tyr Val Phe Gly Asp Cys Val Gln Gly Asp Trp Cys Pro Ile Ser
20 25 30

Gly Gly Leu Cys Ser Ala Arg Leu His Arg His Ala Leu Leu Ala Thr
35 40 45

Cys Pro Glu His Gln Ile Thr Trp Asp Pro Ile Asp Gly Arg Val Ile
50 55 60

Gly Ser Ala Leu Gln Phe Leu Ile Pro Arg Leu Pro Ser Phe Pro Thr
65 70 75 80

Gln Arg Thr Ser Lys Thr Leu Lys Val Leu Thr Pro Pro Ile Thr His
85 90 95

Thr Thr Pro Asn Ile Pro Pro Ser Phe Leu Gln Ala Met Arg Lys Tyr
100 105 110

Ser Pro Phe Arg Asn Gly Tyr Met Glu Pro Thr Leu Gly Gln His Leu
115 120 125

Pro Thr Leu Ser Phe Pro Asp Pro Gly Leu Arg Pro Gln Asn Leu Tyr
130 135 140

Thr Leu Trp Gly Gly Ser Val Val Cys Met Tyr Leu Tyr Gln Leu Ser
145 150 155 160

Pro Pro Ile Thr Trp Pro Leu Leu Pro His Val Ile Phe Cys His Pro
165 170 175

Gly Gln Leu Gly Ala Phe Leu Thr Asn Val Pro Tyr Lys Arg Ile Glu
180 185 190

Glu Leu Leu Tyr Lys Ile Ser Leu Thr Thr Gly Ala Leu Ile Ile Leu
195 200 205

Pro Glu Asp Cys Leu Pro Thr Thr Leu Phe Gln Pro Val Arg Ala Pro
210 215 220

warf Sequence.ST25.txt

Val Thr Leu Thr Ala Trp Gln Asn Gly Leu Leu Pro Phe His Ser Thr
225 230 235 240

Leu Thr Thr Pro Gly Leu Ile Trp Thr Phe Thr Asp Gly Thr Pro Met
245 250 255

Ile Ser Gly Pro Cys Pro Lys Asp Gly Gln Pro Ser Leu Val Leu Gln
260 265 270

Ser Ser Ser Phe Ile Phe His Lys Phe Gln Thr Lys Ala Tyr His Pro
275 280 285

Ser Phe Leu Leu Ser His Gly Leu Ile Gln Tyr Ser Ser Phe His Asn
290 295 300

Leu His Leu Leu Phe Glu Glu Tyr Thr Asn Ile Pro Ile Ser Leu Leu
305 310 315 320

Phe Asn Lys Lys Glu Ala Asp Asp Asn Asp His Glu Pro Gln Ile Ser
325 330 335

Pro Gly Gly Leu Glu Pro Pro Ser Glu Lys His Phe Arg Glu Thr Glu
340 345 350

Val

<210> 13

<211> 101

<212> PRT

<213> Human T-cell lymphotropic virus type 1

<400> 13

Met Glu Pro Val Asp Pro Asn Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Arg Thr Ala Cys Asn Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Tyr Ala Cys Phe Thr Arg Lys Gly Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro Gln Asp Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln Pro Ala Ser Gln Ser Arg Gly Asp
65 70 75 80

warf Sequence.ST25.txt

Pro Thr Gly Pro Thr Glu Ser Lys Lys Lys Val Glu Arg Glu Thr Glu
85 90 95

Thr Asp Pro Phe Asp
100

<210> 14
<211> 7685
<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

<220>
<221> LTR
<222> (149)..(737)
<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1753)..(2148)
<223> Blasticidin Resistance

<220>
<221> promoter
<222> (2257)..(3074)
<223> CMV IE promoter

<220>
<221> misc_recomb
<222> (3078)..(3102)
<223> attB1

<220>
<221> CDS
<222> (3115)..(4041)
<223> BLV Tax

<220>
<221> misc_recomb
<222> (4046)..(4070)
<223> attB2

<220>
<221> misc_signal
<222> (4082)..(4674)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory element

<220>
<221> LTR
<222> (4720)..(5313)
<223> 3' MoMuLVLTR

<220>
<221> CDS
<222> (6616)..(7476)
<223> Ampicillin Resistance

Warf Sequence.ST25.txt

<400> 14	gaattaaattc ataccagatc accgaaaact gtcctccaaa tgtgtcccccc tcacactccc	60
aaattcgcgg gcttctgcct cttagaccac tctaccctat tccccacact caccggagcc	120	
aaagccgcgg cccttccgtt tctttgctt tgaaagaccc caccctgttgg tggcaagcta	180	
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cgtctgaatt tttgcttcg gtttggaaacc gaagccgcgc gtcttgcgtc ctgcagcgct	1140	
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gttcgaccccg gcctcgatcc tccctttatc cagccctcac tccttctcta ggccggaa	1620	
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gcacgtgttgc acaattaatc atcggcatag tatatcgca tagtataata cgacaagggt	1740	
aggaactaaa cc atg gcc aag cct ttg tct caa gaa gaa tcc acc ctc att	1791	
Met Ala Lys Pro Leu Ser Gln Glu Glu Ser Thr Leu Ile		
1 5 10		

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gaa aga gca acg gct aca atc aac agc atc ccc atc tct gaa gac tac Glu Arg Ala Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr 15 20 25	1839
agc gtc gcc agc gca gct ctc tct agc gac ggc cgc atc ttc act ggt Ser Val Ala Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly 30 35 40 45	1887
gtc aat gta tat cat ttt act ggg gga cct tgt gca gaa ctc gtg gtg Val Asn Val Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val 50 55 60	1935
ctg ggc act gct gct gcg gca gct ggc aac ctg act tgt atc gtc Leu Gly Thr Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val 65 70 75	1983
gcg atc gga aat gag aac agg ggc atc ttg agc ccc tgc gga cgg tgt Ala Ile Gly Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys 80 85 90	2031
cga cag gtg ctt ctc gat ctg cat cct ggg atc aaa gcg ata gtg aag Arg Gln Val Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys 95 100 105	2079
gac agt gat gga cag ccg acg gca gtt ggg att cgt gaa ttg ctg ccc Asp Ser Asp Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro 110 115 120 125	2127
tct ggt tat gtg tgg gag ggc taagcacttc gtggccgagg agcaggactg Ser Gly Tyr Val Trp Glu Gly 130	2178
acacgtgcta cgagatttcg attccaccgc cgcctttat gaaaggttgg gcttcggaat	2238
cgtttccgg gacgccgatc cggccattag ccatattatt cattggttat atagcataaa	2298
tcaatattgg ctattggcca ttgcatacgt tgtatccata tcataatatg tacattata	2358
ttggctcatg tccaaacatta ccgccatgtt gacattgatt attgactagt tattaatagt	2418
aatcaattac ggggtcatta gttcatagcc catatatgga gttccgcgtt acataactta	2478
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cgtatgttcc catagtaacg ccaataggga ctttccattg acgtcaatgg gtggagtatt	2598
tacggtaaac tgcccacttg gcagtacatc aagtgtatca tatgccaagt acgcccccta	2658
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actttcctac ttggcagtac atctacgtat tagtcatgc tattaccatg gtgatgcggt	2778
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accccattga cgtcaatggg agtttgggg ggcaccaaaa tcaacgggac tttccaaaat	2898
gtcgtaacaa ctccgccccca ttgacgcaaa tgggcggtag gcatgtacgg tgggaggtct	2958
atataagcag agctcgaaa gtgaaccgtc agatcgccgt gagacgccat ccacgctgtt	3018
ttgacaccttca tagaagacac cgggaccgt ccagcctccg cggccccaag cttgttatca	3078

Warf Sequence.ST25.txt

caagttgtcaaaaaagca ggctccgcgcc accatgtgttgg	3132
Met Ala Ser Val Val Gly	
135	
tgg ggg ccc cac tct cta cat gcc tgc ccg gcc ctg gtt ttg tcc aat	3180
Trp Gly Pro His Ser Leu His Ala Cys Pro Ala Leu Val Leu Ser Asn	
140 145 150	
gat gtc acc atc gat gcc tgg tgc ccc ctc tgc ggg ccc cat gag cga	3228
Asp Val Thr Ile Asp Ala Trp Cys Pro Leu Cys Gly Pro His Glu Arg	
155 160 165 170	
ctc caa ttc gaa agg atc gac acc acg ctc acc tgc gag acc cac cgt	3276
Leu Gln Phe Glu Arg Ile Asp Thr Thr Leu Thr Cys Glu Thr His Arg	
175 180 185	
atc aac tgg acc gcc gat gga cga cct tgc ggc ctc aat gga acg ttg	3324
Ile Asn Trp Thr Ala Asp Gly Arg Pro Cys Gly Leu Asn Gly Thr Leu	
190 195 200	
ttc cct cga ctg cat gtc tcc gag acc cgc ccc caa ggg ccc cga cga	3372
Phe Pro Arg Leu His Val Ser Glu Thr Arg Pro Gln Gly Pro Arg Arg	
205 210 215	
ctc tgg atc aac tgc ccc ctt ccg gcc gtt cgc gct cag ccc ggc ccg	3420
Leu Trp Ile Asn Cys Pro Leu Pro Ala Val Arg Ala Gln Pro Gly Pro	
220 225 230	
gtt tca ctt tcc ccc ttc gag cgg tcc ccc ttc cag ccc tac caa tgc	3468
Val Ser Leu Ser Pro Phe Glu Arg Ser Pro Phe Gln Pro Tyr Gln Cys	
235 240 245 250	
caa ttg ccc tcg gcc tct agc gac ggt tgc ccc att atc ggg cac ggc	3516
Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys Pro Ile Ile Gly His Gly	
255 260 265	
ctt ctt ccc tgg aac aac tta gta acg cat cct gtc ctc aga aaa gtc	3564
Leu Leu Pro Trp Asn Asn Leu Val Thr His Pro Val Leu Arg Lys Val	
270 275 280	
ctt ata tta aatcaa atg gcc aat ttt tcc tta ctc ccc tcc ttc gat	3612
Leu Ile Leu Asn Gln Met Ala Asn Phe Ser Leu Leu Pro Ser Phe Asp	
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acc ctc ctt gtg gac ccc ctc cgg ctg tcc gtc ttt gcc cca gac acc	3660
Thr Leu Leu Val Asp Pro Leu Arg Leu Ser Val Phe Ala Pro Asp Thr	
300 305 310	
agg gga gcc ata cgt tat ctc tcc acc ctt ttg acg cta tgc ccg gct	3708
Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu Leu Thr Leu Cys Pro Ala	
315 320 325 330	
act tgt att cta ccc cta ggc gag ccc ttc tct cct aat gtc ccc ata	3756
Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe Ser Pro Asn Val Pro Ile	
335 340 345	
tgc cgc ttt ccc cgg gac tcc aat gaa ccc ccc ctt tca gaa ttc gag	3804
Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro Pro Leu Ser Glu Phe Glu	
350 355 360	
ctg ccc ctt atc caa acg ccc ggc ctg tct tgg tct gtc ccc gcg atc	3852
Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser Trp Ser Val Pro Ala Ile	
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Warf Sequence.ST25.txt

gac cta ttc cta acc ggt ccc cct tcc cca tgc gac cgg tta cac gta	3900
Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro Cys Asp Arg Leu His Val	
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Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe Leu His Asp Pro Thr Leu	
395 400 405 410	
acc tgg tcc gaa tta gtt gct agc aga aaa ata aga ctt gat tcc ccc	3996
Thr Trp Ser Glu Leu Val Ala Ser Arg Lys Ile Arg Leu Asp Ser Pro	
415 420 425	
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Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp Leu Ser Arg Leu Phe	
430 435 440	
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warf Sequence.ST25.txt

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cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg tct att tcg	6666
Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser	
445 450 455	

ttc atc cat agt tgc ctg act ccc cgt cgt gta gat aac tac gat acg	6714
Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr	
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Gly Gly Leu Thr Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro	
475 480 485	

acg ctc acc ggc tcc aga ttt atc agc aat aaa cca gcc agc cgg aag	6810
Thr Leu Thr Gly Ser Arg Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys	
490 495 500 505	

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Gly Arg Ala Gln Lys Trp Ser Cys Asn Phe Ile Arg Leu His Pro Val	
510 515 520	

tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc agt taa tag	6906
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Warf Sequence.ST25.txt

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Phe	Ala	Gln	Arg	Cys	Cys	His	Cys	Cys	Arg	His	Arg	Gly	Val	Thr	Leu	
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gtc	gtt	tgg	tat	ggc	tcc	att	cag	ctc	cgg	tcc	cca	acg	atc	aag	gct	7002
Val	Val	Trp	Tyr	Gly	Phe	Ile	Gln	Leu	Arg	Phe	Pro	Thr	Ile	Lys	Ala	
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Ser	Tyr	Met	Ile	Pro	His	Val	Val	Gln	Lys	Ser	Gly		Leu	Leu	Arg	
565				570					575							
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Ser	Ser	Asp	Arg	Cys	Gln	Lys		Val	Gly	Arg	Ser	Val	Ile	Thr	His	
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ggt	tat	ggc	agc	act	gca	taa	tcc	tct	tac	tgt	cat	gcc	atc	cgt	aag	7146
Gly	Tyr	Gly	Ser	Thr	Ala		Phe	Ser	Tyr	Cys	His	Ala	Ile	Arg	Lys	
595				600					605							
atg	ctt	tcc	tgt	gac	tgg	tga	gtc	ctc	aac	caa	gtc	att	ctg	aga	ata	7194
Met	Leu	Phe	Cys	Asp	Trp		Val	Leu	Asn	Gln	Val	Ile	Leu	Arg	Ile	
610				615					620							
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Val	Tyr	Ala	Ala	Thr	Glu	Leu	Leu	Leu	Pro	Gly	Val	Asn	Thr	Gly		
625				630					635							
tac	cgc	gcc	aca	tag	cag	aac	ttt	aaa	agt	gct	cat	cat	tgg	aaa	acg	7290
Tyr	Arg	Ala	Thr		Gln	Asn	Phe	Lys	Ser	Ala	His	His	Trp	Lys	Thr	
640					645					650						
ttc	ttc	ggg	gct	aaa	act	ctc	aag	gat	ctt	acc	gct	gtt	gag	atc	cag	7338
Phe	Phe	Gly	Ala	Lys	Thr	Leu	Lys	Asp	Leu	Thr	Ala	Val	Glu	Ile	Gln	
655				660					665				670			
ttc	gat	gta	acc	cac	tcg	tgc	acc	caa	ctg	atc	tcc	agc	atc	ttt	tac	7386
Phe	Asp	Val	Thr	His	Ser	Cys	Thr	Gln	Leu	Ile	Phe	Ser	Ile	Phe	Tyr	
675					680					685						
ttt	cac	cag	cgt	ttc	tgg	gtg	agc	aaa	aac	agg	aag	gca	aaa	tgc	cgc	7434
Phe	His	Gln	Arg	Phe	Trp	Val	Ser	Lys	Asn	Arg	Lys	Ala	Lys	Cys	Arg	
690				695					700							
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Lys	Lys	Gly	Asn	Lys	Gly	Asp	Thr	Glu	Met	Leu	Asn	Thr	His			
705				710					715							
act	tttc	cctt	tttca	att	tttca	atttt	tttca	tttca	tttca	7536						
cat	at	ttt	tttca	tttca	tttca	7596										
agt	tttca	tttca	tttca	7656												
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warf Sequence.ST25.txt

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<220>

<223> Synthetic Construct

<400> 15

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Thr Ala Thr Ile Asn Ser Ile Pro Ile Ser Glu Asp Tyr Ser Val Ala
20 25 30

Ser Ala Ala Leu Ser Ser Asp Gly Arg Ile Phe Thr Gly Val Asn Val
35 40 45

Tyr His Phe Thr Gly Gly Pro Cys Ala Glu Leu Val Val Leu Gly Thr
50 55

Ala Ala Ala Ala Ala Ala Gly Asn Leu Thr Cys Ile Val Ala Ile Gly
65 70 75 80

Asn Glu Asn Arg Gly Ile Leu Ser Pro Cys Gly Arg Cys Arg Gln Val
85 90 95

Leu Leu Asp Leu His Pro Gly Ile Lys Ala Ile Val Lys Asp Ser Asp
100 105 110

Gly Gln Pro Thr Ala Val Gly Ile Arg Glu Leu Leu Pro Ser Gly Tyr
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Val Trp Glu Gly
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<211> 309

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 16

Met Ala Ser Val Val Gly Trp Gly Pro His Ser Leu His Ala Cys Pro
1 5 10 15

Ala Leu Val Leu Ser Asn Asp Val Thr Ile Asp Ala Trp Cys Pro Leu
20 25 30

Cys Gly Pro His Glu Arg Leu Gln Phe Glu Arg Ile Asp Thr Thr Leu
35 40 45

warf Sequence.ST25.txt

Thr Cys Glu Thr His Arg Ile Asn Trp Thr Ala Asp Gly Arg Pro Cys
50 55 60

Gly Leu Asn Gly Thr Leu Phe Pro Arg Leu His Val Ser Glu Thr Arg
65 70 75 80

Pro Gln Gly Pro Arg Arg Leu Trp Ile Asn Cys Pro Leu Pro Ala Val
85 90 95

Arg Ala Gln Pro Gly Pro Val Ser Leu Ser Pro Phe Glu Arg Ser Pro
100 105 110

Phe Gln Pro Tyr Gln Cys Gln Leu Pro Ser Ala Ser Ser Asp Gly Cys
115 120 125

Pro Ile Ile Gly His Gly Leu Leu Pro Trp Asn Asn Leu Val Thr His
130 135 140

Pro Val Leu Arg Lys Val Leu Ile Leu Asn Gln Met Ala Asn Phe Ser
145 150 155 160

Leu Leu Pro Ser Phe Asp Thr Leu Leu Val Asp Pro Leu Arg Leu Ser
165 170 175

Val Phe Ala Pro Asp Thr Arg Gly Ala Ile Arg Tyr Leu Ser Thr Leu
180 185 190

Leu Thr Leu Cys Pro Ala Thr Cys Ile Leu Pro Leu Gly Glu Pro Phe
195 200 205

Ser Pro Asn Val Pro Ile Cys Arg Phe Pro Arg Asp Ser Asn Glu Pro
210 215 220

Pro Leu Ser Glu Phe Glu Leu Pro Leu Ile Gln Thr Pro Gly Leu Ser
225 230 235 240

Trp Ser Val Pro Ala Ile Asp Leu Phe Leu Thr Gly Pro Pro Ser Pro
245 250 255

Cys Asp Arg Leu His Val Trp Ser Ser Pro Gln Ala Leu Gln Arg Phe
260 265 270

Leu His Asp Pro Thr Leu Thr Trp Ser Glu Leu Val Ala Ser Arg Lys
275 280 285

Ile Arg Leu Asp Ser Pro Leu Lys Leu Gln Leu Leu Glu Asn Glu Trp

Warf Sequence.ST25.txt

290

295

300

Leu Ser Arg Leu Phe
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<400> 17

Leu Pro Met Leu Asn Gln
 1 5

<210> 18
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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 18

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
 20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
 35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
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Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
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<400> 19

Leu Leu Pro Gly Ser
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warf Sequence.ST25.txt

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<400> 20

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Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
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Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
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<400> 21

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<210> 23
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 23

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
Page 22

1 5 10 15
warf Sequence.ST25.txt

<210> 24
<211> 24
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 24

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<212> PRT
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<223> Synthetic Construct

<400> 25

Tyr Arg Ala Thr
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<210> 26
<211> 73
<212> PRT
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<220>
<223> Synthetic Construct

<400> 26

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
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Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70

Worf Sequence.ST25.txt

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<211> 7430
<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

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<221> LTR
<222> (1)..(589)
<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1512)..(2306)
<223> neomycin resistance

<220>
<221> misc_feature
<222> (3023)..(3047)
<223> attB1

<220>
<221> CDS
<222> (3120)..(3590)
<223> trans-dominant BLV Rex (M4)

<220>
<221> misc_feature
<222> (3653)..(4282)
<223> attB2

<220>
<221> misc_signal
<222> (3690)..(4282)
<223> WPRE; woodchuck hepatitis virus post-transcriptional regulatory element

<220>
<221> LTR
<222> (4328)..(4921)
<223> 3' MoMuLVLTR

<220>
<221> CDS
<222> (6217)..(7077)
<223> ampicillin resistance

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Warf Sequence.ST25.txt

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Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala		
1 5 10		
gct tgg gtg gag agg cta ttc ggc tat gac tgg gca caa cag aca atc		1598
Ala Trp Val Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile		
15 20 25		
ggc tgc tct gat gcc gcc gtg ttc cgg ctg tca gcg cag ggg cgc ccg		1646
Gly Cys Ser Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro		
30 35 40 45		
gtt ctt ttt gtc aag acc gac ctg tcc ggt gcc ctg aat gaa ctg cag		1694
Val Leu Phe Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln		
50 55 60		
gac gag gca gcg cgg cta tcg tgg ctg gcc acg acg ggc gtt cct tgc		1742
Asp Glu Ala Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys		
65 70 75		
gca gct gtg ctc gac gtt gtc act gaa gcg gga agg gac tgg ctg cta		1790
Ala Ala Val Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu		
80 85 90		

warf Sequence.ST25.txt

ttg ggc gaa gtg ccg ggg cag gat ctc ctg tca tct cac ctt gct cct Leu Gly Glu Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro 95 100 105	1838
gcc gag aaa gta tcc atc atg gct gat gca atg cg ^g cg ^g ctg cat acg Ala Glu Lys Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr 110 115 120 125	1886
ctt gat ccg gct acc tgc cca ttc gac cac caa gcg aaa cat cgc atc Leu Asp Pro Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile 130 135 140	1934
gag cga gca cgt act cg ^g atg gaa gcc ggt ctt gtc gat cag gat gat Glu Arg Ala Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp 145 150 155	1982
ctg gac gaa gag cat cag ggg ctc gcg cca gcc gaa ctg ttc gcc agg Leu Asp Glu Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg 160 165 170	2030
ctc aag gcg cgc atg ccc gac ggc gag gat ctc gtc gtg acc cat ggc Leu Lys Ala Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly 175 180 185	2078
gat gcc tgc ttg ccg aat atc atg gtg gaa aat ggc cgc ttt tct gga Asp Ala Cys Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly 190 195 200 205	2126
ttc atc gac tgt ggc cg ^g ctg ggt gtg gcg gac cgc tat cag gac ata Phe Ile Asp Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile 210 215 220	2174
g ^c g ttg gct acc cgt gat att gct gaa gag ctt ggc ggc gaa tgg gct Ala Leu Ala Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala 225 230 235	2222
gac cgc ttc ctc gtg ctt tac ggt atc gcc gct ccc gat tcg cag cgc Asp Arg Phe Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg 240 245 250	2270
atc gcc ttc tat cgc ctt ctt gac gag ttc ttc tga gcgggactct Ile Ala Phe Tyr Arg Leu Leu Asp Glu Phe Phe 255 260	2316
ggggttcgaa atgaccgacc aagc ^g acg ^{cc} caac ^c tcg ^{cc} tcac ^g agatt tcgattccac cgccgc ^c ttc tatgaaagg ^t tgggcttcgg aatcg ^t tttc cgggacg ^{cc} cg gctggatgat cctccagcgc gggatctca tgctggagtt cttcgcc ^{cc} ac cccgggctcg atccc ^c tcgc gagttgg ^t tc agctgctg ^{cc} tgaggctg ^{ga} cgac ^c tcg ^{cg} gagttctacc ggc ^c agtgc ^{aa} atccgtc ^{gg} c atccaggaaa ccagc ^g acg ^{cg} c ^t atccg ^c gc ^c atccatg ^{ccc} ccgaactg ^{ca} ggagtggg ^{ga} ggc ^c acgatgg c ^c gc ^c tttgg ^t cgaggc ^{gg} at cctagc ^g agaa aaataagact tgattcccc ^c taaaattac aactgctaga aatgaatgg ctctccc ^g cc tttttgagg ggaaatcatt t ^t gtatgaaag atcatg ^c ccga cctaggc ^g cc g ^c caccg ^{cc} cc cgtaaaccag acagagacgt cagctg ^c ccag aaaagctg ^{gt} gacggc ^g agct ggtggctaga atccccgtac	2376 2436 2496 2556 2616 2676 2736 2796 2856

Warf Sequence.ST25.txt

ctcccccaact tcccctttcc cgaaaaatcc acaccctgag ctgctgaccc cacctgctga	2916
taaattaata aaatgccggc cctgtcgagt tagcggcacc agaagcgttc ttctcctgag	2976
accctcgta tcagctctcg gtcctgcctc gagaagcttg ttatcaacaa gtttgtacaa	3036
aaaagcaggc ttcgaaggag atagaaccaa ttctctaagg aaatacttaa cgtcgactgg	3096
atccggtacc gaattcgatc cac atg cct aaa aaa cga cgg tcc cga aga cgc Met Pro Lys Lys Arg Arg Ser Arg Arg Arg	3149
265 270	
cca caa ccg atc atc aga tgg caa gtg ttg gtt ggg ggc ccc act Pro Gln Pro Ile Ile Arg Trp Gln Val Leu Leu Val Gly Gly Pro Thr	3197
275 280 285 290	
ctc tac atg cct gcc cgg ccc tgg ttt tgt cca atg atg tca cca tcg Leu Tyr Met Pro Ala Arg Pro Trp Phe Cys Pro Met Met Ser Pro Ser	3245
295 300 305	
atg cct ggt gcc ccc tct gcg ggc ccc atg agc gac tcc aat tcg aaa Met Pro Gly Ala Pro Ser Ala Gly Pro Met Ser Asp Ser Asn Ser Lys	3293
310 315 320	
gga tcg aca cca cgc tca cct gcg aga ccc acc gta tca act gga ccg Gly Ser Thr Pro Arg Ser Pro Ala Arg Pro Thr Val Ser Thr Gly Pro	3341
325 330 335	
ccg atg gac gac ctt gcg gcc tca atg gaa cgt tgt tcc ctc gac tgc Pro Met Asp Asp Leu Ala Ala Ser Met Glu Arg Cys Ser Leu Asp Cys	3389
340 345 350	
atg tct ccg aga ccc gcc ccc aag ggc ccc gac gac tct gga tca act Met Ser Pro Arg Pro Ala Pro Lys Gly Pro Asp Asp Ser Gly Ser Thr	3437
355 360 365 370	
gcc ccc ttc cgg ccg ttc gcg ctc agc ccg gcc cggtt aat gat ctt ccc Ala Pro Phe Arg Pro Phe Ala Leu Ser Pro Ala Arg Leu Asp Leu Pro	3485
375 380 385	
cct tcg agc ggt ccc cct tcc agc cct acc aat gcc aat tgc cct ccg Pro Ser Ser Gly Pro Pro Ser Ser Pro Thr Asn Ala Asn Cys Pro Arg	3533
390 395 400	
cct cta gcg acg gtt gcc cca tta tcg ggc acg gcc ttc ttc cct gga Pro Leu Ala Thr Val Ala Pro Leu Ser Gly Thr Ala Phe Phe Pro Gly	3581
405 410 415	
aca act tag taacgcatcc tgtcctcaga aaagtccctta tattaaatca	3630
Thr Thr	
420	
aatgggacct cgagatatct agacccagct ttcttgtaca aagtgggtga taacatcgat	3690
aatcaacctc tggattacaa aatttgtgaa agattgactg gtattcttaa ctatgttgct	3750
cctttacgc tatgtggata cgctgctta atgccttgc atcatgctat tgcttcccgat	3810
atggcttca ttttctccctc cttgtataaa tcctgggtgc tgtctctta tgaggagttg	3870
tggcccggttgc tcaggcaacg tggcgtggtg tgcaactgtgt ttgctgacgc aaccccccact	3930
gttggggca ttgccaccac ctgtcagctc cttccggga ctttcgcttt cccccccct	3990

Warf Sequence.ST25.txt

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aatccagcgg	accttccttc	ccgcggcctg	ctgcccgtc	tgccggctct	tccgcgtctt	4230
cgccttcgcc	ctcagacgag	tcggatctcc	ctttggccg	cctccccgcc	tgatcgataa	4290
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gcccgaccgc	tgcgccttat	ccggtaacta	tcgtctttag	tccaacccgg	taagacacga	5790
cttacgcaca	ctggcagcag	ccactggtaa	caggattagc	agagcggaggt	atgttaggcgg	5850

warf Sequence.ST25.txt

tgctacagag ttcttgaagt ggtggcctaa ctacggctac actagaagga cagtattgg	5910
tatctgcgt ctgctgaagc cagttacctt cgaaaaaaga gttggtagct cttgatccgg	5970
caaacaacc accgctggta gcgggtgtt tttgtttgc aagcagcaga ttacgcgcag	6030
aaaaaaagga tctcaagaag atcctttgat ctttctacg gggctgacg ctcagtggaa	6090
cgaaaaactca cgtaaggga tttggtcat gagattatca aaaaggatct tcacctagat	6150
cctttaaat taaaaatgaa gttttaaatc aatctaaagt atatatgagt aaacttggtc	6210
tgacag tta cca atg ctt aat cag tga ggc acc tat ctc agc gat ctg	6258
Leu Pro Met Leu Asn Gln Gly Thr Tyr Leu Ser Asp Leu	
425 430	
tct att tcg ttc atc cat agt tgc ctg act ccc cgt cgt gta gat aac	6306
Ser Ile Ser Phe Ile His Ser Cys Leu Thr Pro Arg Arg Val Asp Asn	
435 440 445	
tac gat acg gga ggg ctt acc atc tgg ccc cag tgc tgc aat gat acc	6354
Tyr Asp Thr Gly Gly Leu Thr Ile Trp Pro Gln Cys Cys Asn Asp Thr	
450 455 460 465	
gcg aga ccc acg ctc acc ggc tcc aga ttt atc agc aat aaa cca gcc	6402
Ala Arg Pro Thr Leu Thr Gly Ser Arg Phe Ile Ser Asn Lys Pro Ala	
470 475 480	
agc cgg aag ggc cga gcg cag aag tgg tcc tgc aac ttt atc cgc ctc	6450
Ser Arg Lys Gly Arg Ala Gln Lys Trp Ser Cys Asn Phe Ile Arg Leu	
485 490 495	
cat cca gtc tat taa ttg ttg ccg gga agc tag agt aag tag ttc gcc	6498
His Pro Val Tyr Leu Leu Pro Gly Ser Ser Lys Phe Ala	
500 505 510	
agt taa tag ttt gcg caa cgt tgt tgc cat tgc tgc agg cat cgt ggt	6546
Ser Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly	
515 520	
gtc acg ctc gtc gtt tgg tat ggc ttc att cag ctc cgg ttc cca acg	6594
Val Thr Leu Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr	
525 530 535 540	
atc aag gcg agt tac atg atc ccc cat gtt gtg caa aaa agc ggt tag	6642
Ile Lys Ala Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly	
545 550 555	
ctc ctt cgg tcc tcc gat cgt tgt cag aag taa gtt ggc cgc agt gtt	6690
Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys Val Gly Arg Ser Val	
560 565 570	
atc act cat ggt tat ggc agc act gca taa ttc tct tac tgt cat gcc	6738
Ile Thr His Gly Tyr Gly Ser Thr Ala Phe Ser Tyr Cys His Ala	
575 580 585	
atc cgt aag atg ctt ttc tgt gac tgg tga gta ctc aac caa gtc att	6786
Ile Arg Lys Met Leu Phe Cys Asp Trp Val Leu Asn Gln Val Ile	
590 595 600	
ctg aga ata gtg tat gcg gcg acc gag ttg ctc ttg ccc ggc gtc aac	6834
Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu Leu Leu Pro Gly Val Asn	
605 610 615	

warf sequence.ST25.txt

acg gga taa tac cgc gcc aca tag cag aac ttt aaa agt gct cat cat	6882
Thr Gly Tyr Arg Ala Thr Gln Asn Phe Lys Ser Ala His His	
620 625 630	
tgg aaa acg ttc ttc ggg gcg aaa act ctc aag gat ctt acc gct gtt	6930
Trp Lys Thr Phe Phe Gly Ala Lys Thr Leu Lys Asp Leu Thr Ala Val	
635 640 645	
gag atc cag ttc gat gta acc cac tcg tgc acc caa ctg atc ttc agc	6978
Glu Ile Gln Phe Asp Val Thr His Ser Cys Thr Gln Leu Ile Phe Ser	
650 655 660	
atc ttt tac ttt cac cag cgt ttc tgg gtg agc aaa aac agg aag gca	7026
Ile Phe Tyr Phe His Gln Arg Phe Trp Val Ser Lys Asn Arg Lys Ala	
665 670 675	
aaa tgc cgc aaa aaa ggg aat aag ggc gac acg gaa atg ttg aat act	7074
Lys Cys Arg Lys Lys Gly Asn Lys Gly Asp Thr Glu Met Leu Asn Thr	
680 685 690	
cat actttccctt tttcaatatt attgaagcat ttatcagggt tattgtctca	7127
His	
695	
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aaactgtcct ccaaatgtgt ccccctcaca ctccccaaatt cgccggcttc tgcccttttag	7367
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gct	7430

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<211> 264
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 28

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1 5 10 15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50 55 60

warf Sequence.ST25.txt

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 29

<211> 156

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 29

warf Sequence.ST25.txt

Met Pro Lys Lys Arg Arg Ser Arg Arg Arg Pro Gln Pro Ile Ile Arg
1 5 10 15

Trp Gln Val Leu Leu Val Gly Gly Pro Thr Leu Tyr Met Pro Ala Arg
20 25 30

Pro Trp Phe Cys Pro Met Met Ser Pro Ser Met Pro Gly Ala Pro Ser
35 40 45

Ala Gly Pro Met Ser Asp Ser Asn Ser Lys Gly Ser Thr Pro Arg Ser
50 55 60

Pro Ala Arg Pro Thr Val Ser Thr Gly Pro Pro Met Asp Asp Leu Ala
65 70 75 80

Ala Ser Met Glu Arg Cys Ser Leu Asp Cys Met Ser Pro Arg Pro Ala
85 90 95

Pro Lys Gly Pro Asp Asp Ser Gly Ser Thr Ala Pro Phe Arg Pro Phe
100 105 110

Ala Leu Ser Pro Ala Arg Leu Asp Leu Pro Pro Ser Ser Gly Pro Pro
115 120 125

Ser Ser Pro Thr Asn Ala Asn Cys Pro Arg Pro Leu Ala Thr Val Ala
130 135 140

Pro Leu Ser Gly Thr Ala Phe Phe Pro Gly Thr Thr
145 150 155

<210> 30

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 30

Leu Pro Met Leu Asn Gln
1 5

<210> 31

<211> 75

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 31

warf Sequence.ST25.txt

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
1 5 10 15

Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
65 70 75

<210> 32

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 32

Leu Leu Pro Gly Ser
1 5

<210> 33

<211> 44

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 33

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
1 5 10 15

Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
35 40

<210> 34

<211> 10

<212> PRT

<213> Artificial

<220>

warf Sequence.ST25.txt

<223> Synthetic Construct

<400> 34

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 35

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
1 5 10

<210> 36

<211> 15

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 36

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
1 5 10 15

<210> 37

<211> 24

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 37

Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu
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Leu Leu Pro Gly Val Asn Thr Gly
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<210> 38

<211> 4

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 38

Warf Sequence.ST25.txt

Tyr Arg Ala Thr
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<210> 39
<211> 73
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 39

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70

<210> 40
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<212> DNA
<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

<220>
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<222> (149)..(737)
<223> 5' MoMuSVLTR

<220>
<221> CDS
<222> (1660)..(2454)
<223> neomycin resistance

<220>
<221> promoter
<222> (2806)..(3150)
<223> BLV promoter

<220>
<221> misc_feature
<222> (3170)..(3194)
<223> attb1

warf Sequence.ST25.txt

<220>
<221> CDS
<222> (3236)..(3955)
<223> EYFP; enhanced yellow fluorescent protein

<220>
<221> misc_feature
<222> (3980)..(4004)
<223> attb2

<220>
<221> LTR
<222> (4056)..(4649)
<223> 3' MoMuSVLTR

<220>
<221> CDS
<222> (5945)..(6805)
<223> ampicillin resistance

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gccagactgt taccactccc ttaagttga ccttaggtca ctggaaagat gtcgagcgga 1260

warf Sequence.ST25.txt

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gga ttg cac gca ggt tct ccg gcc gct tgg gtg gag agg cta ttc ggc Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly 10 15 20	1722
tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg ttc Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe 25 30 35	1770
cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac ctg Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu 40 45 50	1818
tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg tgg Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp 55 60 65	1866
ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc act Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr 70 75 80 85	1914
gaa gcg gga agg gac tgg ctg cta ttg ggc gaa gtg ccg ggg cag gat Glu Ala Gly Arg Asp Trp Leu Leu Gly Glu Val Pro Gly Gln Asp 90 95 100	1962
ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala 105 110 115	2010
gat gca atg cgg cgg ctg cat acg ctt gat ccg gct acc tgc cca ttc Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe 120 125 130	2058
gac cac caa gcg aaa cat cgc atc gag cga gca cgt act cgg atg gaa Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu 135 140 145	2106
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu 150 155 160 165	2154
gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac ggc Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly 170 175 180	2202
gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc atg Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met	2250

warf Sequence.ST25.txt

185

190

195

gtg gaa aat ggc cgc ttt tct gga ttc atc gac tgt ggc cgg ctg ggt	2298
Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly	
200 205 210	
gtg gcg gac cgc tat cag gac ata gcg ttg gct acc cgt gat att gct	2346
Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala	
215 220 225	
gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc ctc gtg ctt tac ggt	2394
Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val Leu Tyr Gly	
230 235 240 245	
atc gcc gct ccc gat tcg cag cgc atc gcc ttc tat cgc ctt ctt gac	2442
Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg Leu Leu Asp	
250 255 260	
gag ttc ttc tga gcgggactct ggggttcgaa atgaccgacc aagcgacgccc	2494
Glu Phe Phe	
caacctgcca tcacgagatt tcgattccac cgccgccttc tatgaaaggt tgggcttcgg	2554
aatcgtttc cgggacgccc gctggatgtat cctccagcgc gggatctca tgctggagtt	2614
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cgacctcgcg gagttctacc ggcagtgc aa atccgtccgc atccaggaaa ccagcagcgg	2734
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gagaagcttg ttatcacaag tttgtacaaa aaagcaggct tcgaaggaga tagaaccaat	3214
tctctaagga aatacttaac c atg gtg agc aag ggc gag gag ctg ttc acc	3265
Met Val Ser Lys Gly Glu Glu Leu Phe Thr	
265 270	
ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac	3313
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His	
275 280 285 290	
aag ttc agc gtg tcc ggc gag ggc gag ggc gat ggc acc acc tac ggc aag	3361
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys	
295 300 305	
ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg	3409
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp	
310 315 320	
ccc acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc	3457

warf Sequence.ST25.txt

Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg			
325						330					335							
tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	3505		
Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro			
340					345					350								
gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	3553		
Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn			
355					360					365				370				
tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	3601		
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn			
375						380					385							
cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	3649		
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu			
390						395					400							
ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	3697		
Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met			
405						410					415							
gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	3745		
Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His			
420						425					430							
aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	3793		
Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn			
435						440					445				450			
acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	3841		
Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu			
455							460						465					
agc	tac	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	3889		
Ser	Tyr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His			
470							475						480					
atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	3937		
Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met			
485						490					495							
gac	gag	ctg	tac	aag	taa	agcggccgca	ctcgagat	at	ctagacccag							3985		
Asp	Glu	Leu	Tyr	Lys														
500																		
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cagat	ggaac	actgaaat	at	gg	ccaaaca	gg	at	at	ctgt	gt	gg	tcc	tgt	gg	taa	4225		
gctc	agg	ggcc	aagaac	ag	ac	ag	ct	g	at	tc	gg	tcc	ag	cc	tc	4285		
gc	agtt	cct	cc	cc	gg	ct	ca	gg	cc	at	tc	gg	tcc	ag	cc	tc	4345	
agc	at	ttt	ct	ag	ga	ac	ca	gt	tt	tc	gg	cc	tc	at	cc	tc	4405	
gtgc	c	ttt	att	t	g	a	act	a	cc	t	tc	cg	tc	tt	tc	tg	tc	4465

Worf Sequence.ST25.txt

cccgagctca ataaaagagc ccacaacccc tcactcgaaa cgccagtcct ccgattgact	4525
gagtgcggcg ggtacccgtg tatccaataa acccttgc agttgcattcc gacttgggt	4585
ctcgctgttc cttgggaggg ttcctctga gtgattgact acccgtagc ggggtcttt	4645
catttggggg ctcgtccggg atcgggagac ccctgcccag ggaccaccga cccaccaccg	4705
ggaggttaagc tggctgcctc gcgcgttcg gtatgcgg tgaaaacctc tgacacatgc	4765
agctcccgg aacggtcaca gcttgtctgt aagcggatgc cggagcaga caagccgtc	4825
agggcgcgtc agcgggtgtt ggcgggtgtc gggcgcagc catgaccagg tcacgtacg	4885
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ccatatgcgg tgtgaaatac cgcacagatc cgtaaggaga aaataccgca tcaggcgctc	5005
ttccgcttcc tcgctcactg actcgctgcg ctcggcggtt cggctgcggc gagcggtac	5065
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catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcg	5185
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cgtggcgctt tctcatagct cacgctgttag gtatctcagt tcgggttagg tcgttcgtc	5425
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taactacggc tacactagaa ggacagtatt tggtatctgc gctctgctga agccagttac	5665
cttcggaaaa agagttggta gctcttgcgc cggcaaaacca accaccgctg gtagcgg	5725
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gatctttct acggggctcg acgctcagtga aacgaaaac tcacgttaag ggatttgg	5845
catgagatta tcaaaaagga tcttaccta gatccttta aataaaaat gaagttttaa	5905
atcaatctaa agtataatag agtaaacttg gtctgacag tta cca atg ctt aat	5959
Leu Pro Met Leu Asn	
505	
cag tga ggc acc tat ctc agc gat ctg tct att tcg ttc atc cat agt	6007
Gln Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser	
510 515 520	
tgc ctg act ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc	6055
Cys Leu Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr	
525 530 535	
atc tgg ccc cag tgc tgc aat gat acc gcg aga ccc acg ctc acc ggc	6103
Ile Trp Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly	
540 545 550 555	

warf Sequence.ST25.txt

tcc aga ttt atc agc aat aaa cca gcc agc cg ^g aag ggc cga g ^{cg} cag Ser Arg Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln 560 565 570	6151
aag tgg tcc tgc aac ttt atc cgc ctc cat cca gtc tat taa ttg ttg Lys Trp Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr Leu Leu 575 580 585	6199
ccg gga agc tag agt aag tag ttc gcc agt taa tag ttt g ^{cg} caa cgt Pro Gly Ser Ser Lys Phe Ala Ser Phe Ala Gln Arg 590 595	6247
tgt tgc cat tgc tgc agg cat cgt ggt gtc acg ctc gtc gtt tgg tat Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu Val Val Trp Tyr 600 605 610	6295
ggc ttc att cag ctc cgg ttc cca acg atc aag g ^{cg} agt tac atg atc Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala Ser Tyr Met Ile 615 620 625 630	6343
ccc cat gtt gtg caa aaa agc ggt tag ctc ctt cg ^g tcc tcc gat cgt Pro His Val Val Gln Lys Ser Gly Leu Leu Arg Ser Ser Asp Arg 635 640 645	6391
tgt cag aag taa gtt ggc cgc agt gtt atc act cat ggt tat ggc agc Cys Gln Lys Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser 650 655 660	6439
act gca taa ttc tct tac tgt cat gcc atc cgt aag atg ctt ttc tgt Thr Ala Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys 665 670 675	6487
gac tgg tga gta ctc aac caa gtc att ctg aga ata gtg tat g ^{cg} g ^{cg} Asp Trp Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala 680 685 690	6535
acc gag ttg ctc ttg ccc ggc gtc aac acg gga taa tac cgc gcc aca Thr Glu Leu Leu Leu Pro Gly Val Asn Thr Gly Tyr Arg Ala Thr 695 700 705	6583
tag cag aac ttt aaa agt gct cat cat tgg aaa acg ttc ttc ggg g ^{cg} Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala 710 715 720	6631
aaa act ctc aag gat ctt acc gct gtt gag atc cag ttc gat gta acc Lys Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr 725 730 735	6679
cac tcg tgc acc caa ctg atc ttc agc atc ttt tac ttt cac cag cgt His Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg 740 745 750	6727
ttc tgg gtg agc aaa aac agg aag gca aaa tgc cgc aaa aaa ggg aat Phe Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn 755 760 765	6775
aag ggc gac acg gaa atg ttg aat act cat actcttcctt ttcaatatt Lys Gly Asp Thr Glu Met Leu Asn Thr His 770 775	6825
attgaagcat ttatcagggt tattgtctca tgagcggata catattgaa tgtatttaga	6885

warf Sequence.ST25.txt

aaaataaaaca aataggggtt ccgcgcacat ttccccaaa agtgccacct gacgtctaag	6945
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ttcaa	7010

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<213> Artificial

<220>
<223> Synthetic Construct

<400> 41

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1 5 10 15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50 55 60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gln Asp Ala Cys
180 185 190

warf Sequence.ST25.txt

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
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<210> 42
<211> 239
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 42

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

warf Sequence.ST25.txt

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 43

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 43

Leu Pro Met Leu Asn Gln
1 5

<210> 44

<211> 75

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 44

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
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Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

warf Sequence.ST25.txt

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
65 70 75

<210> 45
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 45

Leu Leu Pro Gly Ser
1 5

<210> 46
<211> 44
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 46

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
1 5 10 15

val val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
35 40

<210> 47
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 47

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
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<210> 48
<211> 14
<212> PRT

warf Sequence.ST25.txt

<213> Artificial

<220>

<223> Synthetic Construct

<400> 48

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
1 5 10

<210> 49

<211> 15

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 49

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
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<210> 50

<211> 24

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 50

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Leu Leu Pro Gly Val Asn Thr Gly
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<210> 51

<211> 4

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 51

Tyr Arg Ala Thr
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<210> 52

<211> 73

<212> PRT

<213> Artificial

<220>

warf Sequence.ST25.txt

<223> Synthetic Construct

<400> 52

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70

<210> 53

<211> 7121

<212> DNA

<213> Artificial

<220>
<223> Engineered Sequence from virus and plasmid

<220>

<221> LTR

<222> (149)..(737)

<223> 5' MoMuSVLTR

<220>

<221> CDS

<222> (1660)..(2454)

<223> neomycin resistance

<220>

<221> promoter

<222> (2806)..(3261)

<223> HIV promoter

<220>

<221> misc_feature

<222> (3281)..(3305)

<223> attB1

<220>

<221> CDS

<222> (3347)..(4066)

<223> EYFP; enhanced yellow fluorescent protein

<220>

<221> misc_feature

<222> (4091)..(4115)

<223> attB2

warf Sequence.ST25.txt

<220>
 <221> LTR
 <222> (4167)..(4760)
 <223> 3' MoMuLVLTR

<220>
 <221> CDS
 <222> (6056)..(6916)
 <223> ampicillin resistance

<400> 53		
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atccgaatcg tggctcgcgt gttccttggg agggtctcct ctgagtgtt gactaccac	720	
gacgggggtc tttcatttgg gggctcgtcc gggatttggaa gacccctgcc cagggaccac	780	
cgaccacca ccgggaggtt agctggccag caacttatct gtgtctgtcc gattgtctag	840	
tgtctatgtt tgatgttatg cgcctgcgtc tgtacttagtt agctaacttag ctctgtatct	900	
ggcggacccg tgggtggact gacgagttct gaacacccgg ccgcaaccct gggagacgtc	960	
ccagggactt tggggccgt ttttgggcc cgacctgagg aaggagatcg atgtggatc	1020	
cgaccccggtc aggatatgtt gttctggtag gagacgagaa cctaaaacag ttcccgcctc	1080	
cgtctgaatt tttgctttcg gtttggaaacc gaagccgcgc gtcttgcgtc ctgcagcgct	1140	
gcagcatcgat tctgtgttgt ctctgtctga ctgtgtttct gtattgtct gaaaattagg	1200	
gccagactgt taccactccc ttaagttga ccttaggtca ctggaaagat gtcgagcgga	1260	
tcgctcacaa ccagtcggta gatgtcaaga agagacgttgg gtttacccctc tgctctgcag	1320	
aatggccaac ctttaacgtc ggtatggccgc gagacggcac ctttaaccga gacccatca	1380	
cccaggttaa gatcaaggtc ttttcccttg gcccgcatttgg acacccagac caggtcccct	1440	
acatcgtgac ctggaaagcc ttggcttttg acccccccctc ctgggtcaag ccctttgtac	1500	
accctaagcc tccgcctcct cttccctccat ccggccgcgtc tctccccctt gaacctccctc	1560	

warf Sequence.ST25.txt

gttcgacccc	gcctcgatcc	tcccttatac	cagccctcac	tccttctcta	ggcgccggaa	1620
ttccgatctg	atcaagagac	aggatgagga	tcgtttcgc	atg att gaa caa gat	Met Ile Glu Gln Asp	1674
				1	5	
gga ttg cac gca ggt tct ccg gcc gct tgg gtg gag agg cta ttc ggc						1722
Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val Glu Arg Leu Phe Gly						
10	15	20				
tat gac tgg gca caa cag aca atc ggc tgc tct gat gcc gcc gtg ttc						1770
Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser Asp Ala Ala Val Phe						
25	30	35				
cgg ctg tca gcg cag ggg cgc ccg gtt ctt ttt gtc aag acc gac ctg						1818
Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe Val Lys Thr Asp Leu						
40	45	50				
tcc ggt gcc ctg aat gaa ctg cag gac gag gca gcg cgg cta tcg tgg						1866
Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala Ala Arg Leu Ser Trp						
55	60	65				
ctg gcc acg acg ggc gtt cct tgc gca gct gtg ctc gac gtt gtc act						1914
Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val Leu Asp Val Val Thr						
70	75	80	85			
gaa gcg gga agg gac tgg ctg cta ttg ggc gaa gtg ccg ggg cag gat						1962
Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu Val Pro Gly Gln Asp						
90	95	100				
ctc ctg tca tct cac ctt gct cct gcc gag aaa gta tcc atc atg gct						2010
Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys Val Ser Ile Met Ala						
105	110	115				
gat gca atg cgg cgg ctg cat acg ctt gat ccg gct acc tgc cca ttc						2058
Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro Ala Thr Cys Pro Phe						
120	125	130				
gac cac caa gcg aaa cat cgc atc gag cga gca cgt act ccg atg gaa						2106
Asp His Gln Ala Lys His Arg Ile Glu Arg Ala Arg Thr Arg Met Glu						
135	140	145				
gcc ggt ctt gtc gat cag gat gat ctg gac gaa gag cat cag ggg ctc						2154
Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu Glu His Gln Gly Leu						
150	155	160	165			
gcg cca gcc gaa ctg ttc gcc agg ctc aag gcg cgc atg ccc gac ggc						2202
Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Arg Met Pro Asp Gly						
170	175	180				
gag gat ctc gtc gtg acc cat ggc gat gcc tgc ttg ccg aat atc atg						2250
Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro Asn Ile Met						
185	190	195				
gtg gaa aat ggc cgc ttt tct gga ttc atc gac tgt ggc cgg ctg ggt						2298
Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly Arg Leu Gly						
200	205	210				
gtg gcg gac cgc tat cag gac ata gcg ttg gct acc cgt gat att gct						2346
Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg Asp Ile Ala						
215	220	225				
gaa gag ctt ggc ggc gaa tgg gct gac cgc ttc ctc gtg ctt tac ggt						2394

Worf Sequence.ST25.txt

Glu	Glu	Leu	Gly	Gly	Glu	Trp	Ala	Asp	Arg	Phe	Leu	Val	Leu	Tyr	Gly		
230					235						240				245		
atc	gcc	gct	ccc	gat	tcg	cag	cgc	atc	gcc	ttc	tat	cgc	ctt	ctt	gac	2442	
Ile	Ala	Ala	Pro	Asp	Ser	Gln	Arg	Ile	Ala	Phe	Tyr	Arg	Leu	Leu	Asp		
														250	255		
														260			
gag	ttc	ttc	tga	gcgggactct	ggggttcgaa	atgaccgacc	aagcgcacgccc									2494	
Glu	Phe	Phe															
caacctgcca	tcacgagatt	tcgattccac	cgccgccttc	tatgaaaggt	tgggcttcgg											2554	
aatcgtttc	cgggacgccc	gctggatgtat	cctccagcgc	ggggatctca	tgctggagtt											2614	
cttcgcccac	cccgggctcg	atccctcgc	gagttggttc	agctgctgcc	tgaggctgga											2674	
cgacctcgcg	gagttctacc	ggcagtgc当地	atccgtcggc	atccaggaaa	ccagcagcgg											2734	
ctatccgcgc	atccatgccc	ccgaactgca	ggagtgggga	ggcacgatgg	ccgcttttgt											2794	
cgaggcggat	cctggaaggg	ctaatttgtt	cccaaagaag	acaagagatc	cttgatctgt											2854	
ggatctacca	cacacaaggc	tactccctg	attggcagaa	ttacacacca	gggcccaggga											2914	
tcagatatcc	actgaccttt	ggatggtgct	tcaagctagt	accagtttag	ccagagaagg											2974	
tagaagaggc	caatgaagga	gagaacaaca	gcttgttaca	ccctatgagc	ctgcatggga											3034	
tggaggacgc	ggagaaagaa	gtgttagtgt	ggaggttga	cagcaaacta	gcatttcatc											3094	
acatggcccg	agagctgcat	ccggagttact	acaaagactg	ctgacatcga	gctttctaca											3154	
agggactttc	cgctggggac	tttccaggga	ggcgtggcct	gggcgggact	ggggagtggc											3214	
gtccctcaga	tgctgcatat	aagcagctgc	ttttgcctg	tactgggcct	cgagaagctt											3274	
gttattcacaa	gtttgtacaa	aaaagcaggc	ttcgaaggag	atagaaccaa	ttctctaagg											3334	
aaatacttaa	cc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg		3385	
		Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val			
		265					270						275				
ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc		3433
Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser		
		280				285						290					
gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg		3481
Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu		
		295				300						305					
aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc		3529
Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu		
		310				315						320			325		
gtg	acc	acc	ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac		3577
Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp		
cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac		3625
His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr		
		345				350						355					

warf Sequence.ST25.txt

gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc	3673
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr	
360 365 370	
cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag	3721
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu	
375 380 385	
ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag	3769
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys	
390 395 400 405	
ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag	3817
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys	
410 415 420	
cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	3865
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
425 430 435	
gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	3913
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
440 445 450	
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	3961
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
455 460 465	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	4009
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
470 475 480 485	
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	4057
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
490 495 500	
tac aag taa agcggccgca ctcgagatat ctagacccag ctttcttgta	4106
Tyr Lys	
caaagtggtg ataacatcga taaaataaaa gattttattt agtctccaga aaaagggggg	4166
aatgaaagac cccacctgta gtttggcaa gctagcttaa gtaacgccat tttgcaaggc	4226
atggaaaaat acataactga gaatagagaa gttcagatca aggtcaggaa cagatggaac	4286
agctgaatat gggccaaaca ggatatctgt ggtaagcagt tcctgccccg gctcaggccc	4346
aagaacagat ggaacagctg aatatggcc aaacaggata tctgtggtaa gcagttcctg	4406
ccccggctca gggccaagaa cagatggtcc ccagatgcgg tccagccctc agcagttct	4466
agagaaccat cagatgttc cagggtgccc caaggacctg aaatgaccct gtgccttatt	4526
tgaactaacc aatcagttcg cttctcgctt ctgttcgcgc gcttctgctc cccgagctca	4586
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cttgggaggg tctcctctga gtgattgact acccgtcagc ggggtcttt catttggggg	4766
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Warf Sequence.ST25.txt

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gacggtcaca gcttgtctgt aagcggatgc cgggagcaga caagccgtc agggcgcgtc	4946
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gtatactggc ttaactatgc ggcattcagag cagattgtac tgagagtgc ccatatgcgg	5066
tgtgaaatac cgcacagatg cgtaaggaga aaataccgca tcaggcgctc ttccgcttcc	5126
tcgctcactg actcgctgctg ctcggcggtt cggctgcggc gagcggtatac agctcactca	5186
aaggcggtaa tacggttatc cacagaatca gggataacg cagggaaagaa catgtgagca	5246
aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcggtt tttccatagg	5306
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tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag aagatccccc gatctttct	5906
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tcaaaaagga tcttcaccta gatcctttta aattaaaaat gaagttttaa atcaatctaa	6026
agtatatatg agtaaacttg gtctgacag tta cca atg ctt aat cag tga ggc	6079
Leu Pro Met Leu Asn Gln Gly	
505 510	
acc tat ctc agc gat ctg tct att tcg ttc atc cat agt tgc ctg act	6127
Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu Thr	
515 520 525	
ccc cgt cgt gta gat aac tac gat acg gga ggg ctt acc atc tgg ccc	6175
Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp Pro	
530 535 540	
cag tgc tgc aat gat acc gcg aga ccc acg ctc acc ggc tcc aga ttt	6223
Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg Phe	
545 550 555	
atc agc aat aaa cca gcc agc cgg aag ggc cga gcg cag aag tgg tcc	6271
Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp Ser	
560 565 570	
tgc aac ttt atc cgc ctc cat cca gtc tat taa ttg ttg ccg gga agc	6319
Cys Asn Phe Ile Arg Leu His Pro Val Tyr Leu Leu Pro Gly Ser	

warf Sequence.ST25.txt

575	580	585	
tag agt aag tag ttc gcc agt taa tag ttt gcg caa cgt tgt tgc cat			6367
Ser Lys Phe Ala Ser		Phe Ala Gln Arg Cys Cys His	
590		595	600
tgc tgc agg cat cgt ggt gtc acg ctc gtc gtt tgg tat ggc ttc att			6415
Cys Cys Arg His Arg Gly Val Thr Leu Val Val Trp Tyr Gly Phe Ile			
605		610	615
cag ctc cgg ttc cca acg atc aag gcg agt tac atg atc ccc cat gtt			6463
Gln Leu Arg Phe Pro Thr Ile Lys Ala Ser Tyr Met Ile Pro His Val			
620		625	630
gtg caa aaa agc ggt tag ctc ctt cgg tcc tcc gat cgt tgt cag aag			6511
Val Gln Lys Ser Gly		Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys	
635		640	645
taa gtt ggc cgc agt gtt atc act cat ggt tat ggc agc act gca taa			6559
Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala			
650		655	660
ttc tct tac tgt cat gcc atc cgt aag atg ctt ttc tgt gac tgg tga			6607
Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp			
665		670	675
gta ctc aac caa gtc att ctg aga ata gtg tat gcg gcg acc gag ttg			6655
Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu			
680		685	690
ctc ttg ccc ggc gtc aac acg gga taa tac cgc gcc aca tag cag aac			6703
Leu Leu Pro Gly Val Asn Thr Gly		Tyr Arg Ala Thr Gln Asn	
695		700	705
ttt aaa agt gct cat cat tgg aaa acg ttc ttc ggg gcg aaa act ctc			6751
Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys Thr Leu			
710		715	720
aag gat ctt acc gct gtt gag atc cag ttc gat gta acc cac tcg tgc			6799
Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His Ser Cys			
725		730	735
acc caa ctg atc ttc agc atc ttt tac ttt cac cag cgt ttc tgg gtg			6847
Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe Trp Val			
740		745	750
755			
agc aaa aac agg aag gca aaa tgc cgc aaa aaa ggg aat aag ggc gac			6895
Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys Gly Asp			
760		765	770
acg gaa atg ttg aat act cat actttccctt tttcaatatt attgaagcat			6946
Thr Glu Met Leu Asn Thr His			
775			
ttatcaggg tattgtctca tgagcggata catattgaa tgtat taga aaaataaaca			7006
aataggggtt ccgcgcacat ttccccgaaa agtgccacct gacgtctaag aaaccattat			7066
tatcatgaca ttaacctata aaaataggcg tatcacgagg cccttcgtc ttcaa			7121

Warf Sequence.ST25.txt

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 54

Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
1 5 10 15

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
20 25 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
35 40 45

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
50 55 60

Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
65 70 75 80

Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
85 90 95

Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
100 105 110

Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
115 120 125

Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
130 135 140

Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
145 150 155 160

Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
165 170 175

Arg Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
180 185 190

Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
195 200 205

Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
210 215 220

warf Sequence.ST25.txt

Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
225 230 235 240

Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
245 250 255

Tyr Arg Leu Leu Asp Glu Phe Phe
260

<210> 55
<211> 239
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 55

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

warf Sequence.ST25.txt

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 56

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 56

Leu Pro Met Leu Asn Gln
1 5

<210> 57

<211> 75

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 57

Gly Thr Tyr Leu Ser Asp Leu Ser Ile Ser Phe Ile His Ser Cys Leu
1 5 10 15

Thr Pro Arg Arg Val Asp Asn Tyr Asp Thr Gly Gly Leu Thr Ile Trp
20 25 30

Pro Gln Cys Cys Asn Asp Thr Ala Arg Pro Thr Leu Thr Gly Ser Arg
35 40 45

Phe Ile Ser Asn Lys Pro Ala Ser Arg Lys Gly Arg Ala Gln Lys Trp
50 55 60

Ser Cys Asn Phe Ile Arg Leu His Pro Val Tyr
65 70 75

Warf Sequence.ST25.txt

<210> 58
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 58

Leu Leu Pro Gly Ser
1 5

<210> 59
<211> 44
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 59

Phe Ala Gln Arg Cys Cys His Cys Cys Arg His Arg Gly Val Thr Leu
1 5 10 15

Val Val Trp Tyr Gly Phe Ile Gln Leu Arg Phe Pro Thr Ile Lys Ala
20 25 30

Ser Tyr Met Ile Pro His Val Val Gln Lys Ser Gly
35 40

<210> 60
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 60

Leu Leu Arg Ser Ser Asp Arg Cys Gln Lys
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 61

Val Gly Arg Ser Val Ile Thr His Gly Tyr Gly Ser Thr Ala
1 5 10

warf Sequence.ST25.txt

<210> 62
<211> 15
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 62

Phe Ser Tyr Cys His Ala Ile Arg Lys Met Leu Phe Cys Asp Trp
1 5 10 15

<210> 63
<211> 24
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 63

Val Leu Asn Gln Val Ile Leu Arg Ile Val Tyr Ala Ala Thr Glu Leu
1 5 10 15

Leu Leu Pro Gly Val Asn Thr Gly
20

<210> 64
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 64

Tyr Arg Ala Thr
1

<210> 65
<211> 73
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 65

Gln Asn Phe Lys Ser Ala His His Trp Lys Thr Phe Phe Gly Ala Lys
1 5 10 15

Thr Leu Lys Asp Leu Thr Ala Val Glu Ile Gln Phe Asp Val Thr His
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warf Sequence.ST25.txt
20 25 30

Ser Cys Thr Gln Leu Ile Phe Ser Ile Phe Tyr Phe His Gln Arg Phe
35 40 45

Trp Val Ser Lys Asn Arg Lys Ala Lys Cys Arg Lys Lys Gly Asn Lys
50 55 60

Gly Asp Thr Glu Met Leu Asn Thr His
65 70